

STIC-Biotech/ChemLib

61261

From: Borin, Michael
Sent: Tuesday, February 26, 2002 1:59 PM
To: STIC-Biotech/ChemLib
Subject: Search request: 09/540325

Examiner: M.Borin
CM1 12A01
AU: 1631; Mailbox 12D01

Tel.: 305-4506

RE: 09/5403²³⁵~~25~~; cyanidium nucl. acids

CRFE

Please conduct search of polynucleotide SEQ ID 1 against the commercial and interference databases.

Thank you

Searcher: Paula Sheppard
Phone: 308-4499
Location: _____
Date Picked Up: 3/02/02
Date Completed: 3/04/04
Searcher Prep/Review: 10
Clerical: _____
Online time: 5

TYPE OF SEARCH:

NA Sequences: 1
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST(where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

SUMMARIES

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2	124.2	30.4	729	8	AF370158	AF370158 Arabidops
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C 5	117.8	28.9	11941	8	YSPG972HB	D83995 Eristion yea
6	117.8	28.9	14147	8	SPBC2985	AL391603 S.pombe c
7	110.2	27.0	97911	3	AC091511	AC091511 Leishmani
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9	109.8	26.9	1348	6	AX073298	AX073298 Sequence
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11	106.6	26.1	506	8	CNS01CEH	AL115461 Botrytis
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13	106.6	26.1	540	8	CNS019PV	AL111947 Botrytis
14	106.6	26.1	540	8	CNS01A0A	AL113186 Botrytis
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17	106.6	26.1	540	8	CNS01CVL	AL116041 Botrytis
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20	106.4	26.1	2104	8	SCG9R034W	Z72819 S.cerevisia
21	105	25.7	542	8	CNS019VN	AL112155 Botrytis
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C 23	102.2	24.8	137129	2	HSAC0001236	AC001236 Homo sapi
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32	92	22.5	417	8	AF093540	AF093540 Zee may's
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RESULT 2
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LOCUS Arabidopsis thaliana putative 60S ribosomal protein
DEFINITION (T16K5.260/AT3g49910) mRNA, complete cds.
ACCESSION AF370158
VERSION AF370158.1 GI:13877790

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
COMMENT
JOURNAL
FEATURES
source
gene
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CDS
3'UTR
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Arabidopsis thaliana
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Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 729)
Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K.,
Goldsmith, A.D., Lee, J.M., Quach, H.L., Tang, C.C., Toriumi, M., Yu, G.,
Bower, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y.,
Ishida, J., Jones, T., Kamlya, A., Karlin-Neumann, G., Kawai, J.,
Kim, C., Koesema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M.,
Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M.,
Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and
Theologis, A.
Full Length cDNA of gene T16K5.260/AT3g49910 (GI:6723436)
Unpublished
2 (bases 1 to 729)
Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K.,
Goldsmith, A.D., Lee, J.M., Quach, H.L., Tang, C.C., Toriumi, M., Yu, G.,
Bower, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y.,
Ishida, J., Jones, T., Kamlya, A., Karlin-Neumann, G., Kawai, J.,
Kim, C., Koesema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M.,
Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M.,
Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and
Theologis, A.
Direct Submission
Submitted (18-APR-2001) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL CDNA : 'RIKEN
Arabidopsis Full-length cDNA') : Seki, M., Narusaka, M., Ishida, J.,
Satou, M., Kamlya, A., Sakurai, T., Carninci, P., Kawai, J.,
Hayashizaki, Y. and Shinozaki, K.
The Salk, Stanford, PGEC (SSP) Consortium members carried out the
sequencing and annotation of the RAFL cDNAs: Yamada, K., Liu, S.X.,
Sakano, H., Pham, P.K., Banh, J., Chung, M.K., Goldsmith, A.D.,
Lee, J.M., Quach, H.L., Tang, C.C., Toriumi, M., Yu, G., Bower, L.,
Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Koesema, E.,
Lam, B., Lin, J., Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J.,
Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.
Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to
this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC)
contributed equally to this work as PIs.
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Matches 195; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 96 atgaagatccaaagttgtagctgctgctagaagaagaagaagaacatacttcaa 155
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Db 94063 ATGAGTACAAACCCAGAGTACCTCTTCGCGAAGAACGAGGCTATTTCACA 94122

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QY 396 tctaattgttga 408
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RESULT 4
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LOCUS 108158 bp DNA PLN 01-DEC-1999
DEFINITION Arabidopsis thaliana DNA chromosome 3, BAC clone F3A4.
ACCESSION AL132978
VERSION AL132978.1 GI:6434211
KEYWORDS
SOURCE
ORGANISM
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 108158)
Bargues,M., Collado,M.C., Navarro,P., Terol,J., Perez-Alonso,M.,
Mewes,H.W., Lemcke,K., Mayer,K.F.X., Quetier,F. and Salanoubat,M.
Unpublished
2 (bases 1 to 108158)
EU Arabidopsis sequencing project.
Direct Submission
Submitted (01-DEC-1999) MIPS, at the Max-Planck-Institut fuer
Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
lemcke@mps.biochem.mpg.de, mayer@mps.biochem.mpg.de
Project
Coordinator: Marcel Salanoubat and Francis Quetier, Grouperment
d'Interet Public, Centre National de Sequencage - GENOSCOPE; 2 rue
Gaston Cremlieux, BP191, 91006 Evry Cedex, France;
http://www.genoscope.cns.fr

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REFERENCE
AUTHORS
TITLE
JOURNAL
1 (bases 1 to 11941)
Yanagida,M.
Direct Submission
Submitted (12-MAR-1996) to the DDBJ/EMBL/Genbank databases.
Mitsuhito Yanagida, Kyoto University, Department of Biophysics,
Kitashirakawa-Oiwakecho, Sakyo-ku, Kyoto, Kyoto 606, Japan
(E-mail:katayama@kotoz.btophys.kyoto-u.ac.jp, Tel:075-753-4205,
Fax:075-753-4208)
2 (sites)
Kohnosu,A., Niwa,O., Yano,M., Saitoh,S., Katayama,T., Nagao,K. and
Yanagida,M.
S.pombe chromosome II cosmid 1228 sequence
Unpublished (1996)
Location/Qualifiers
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VERSION	DB3993			
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CDs
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    /note="unnamed protein product"
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    /protein_id="BAAI2201.1"
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    FVSKSVMTKLLTSTSELPARSGTYDEGASVCNESCESSCLSNPKSVALLPNTL"
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    /note="unnamed protein product"
    /codon_start=1
    /protein_id="BAAI2202.1"
    /db_xref="GI:1827512"
    /translation="MLSLAKTRPADXXWSREERTNTNELSNPKCFLELDFEDF
    PHOODLIMKYLAEFSASLEDPNLALMKKOVITSKIGHPLVMPJSSRHCVQRFD
    LVCVOTSTAEFVSVDRELTYDNLTKLXTASRTAONMLFTMHHLIEIVGYLPHX
    AHLKOYSLIDYAKSVEXHPELGTIVORRGFLQSR"

BASE COUNT      3774 a      2224 c      2065 g      3755 t      123 others
ORIGIN

Query Match
Best Local Similarity 61.0%; Score 117.8; DB 8; Length 11941;
Matches 191; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

QY 96 atgaagatccaaagtgtatcgtcgtctagaaagaagcagaagaactattcaa 155
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 4235 ATGAGATTCTCCAGGAGTGTACTAGCTCGTCCAGCAAGCAAGGCTTCATCGGC 4176
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 156 geacacatctctgtcgaagaatactcgaatgacaccttccaaagaactacg 215
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 4175 GCCCCTTCATCTGTACGCGGTGTTAATGCTGCTCTTCCTTCAGAGAGCTTGAGAG 4116
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 216 aatacagcgttcgtcttaccattcgaagaagcagaagtaatactagttcgcgga 275
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 4115 CATACAAATCGTCTCTTCAGTTCGTGATGACCAATACGTCAATCGTGAT 4056
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
*QY 276 gcttcaaggtagaagaagaagtaacagctgttaccgaagaataatcgatcact 335
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 4055 TCCACAAAGGTCGCGAGAGCAAGATCACCTCGTTCACGTAAGAAATTCCTTCTCTT 3996
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 336 atcgaagaaggtagcagaagaagaagaatggaatgacaccttgggaatactca 395
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 3995 ATTGACCGTGTACCCCGCGAAGAGCCAAAGCGCTCTGACACCGCTCGATCGAGCGC 3936
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 396 tctaactgttcta 408
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 3935 TCTAAGGTGTCTCA 3923

RESULT 6
SPBC29B5/c      14147 bp      DNA      PLN      29-AUG-2000
LOCUS      S.pombe chromosome II cosmid c29B5.
DEFINITION      AL391603
VERSION      AL391603.1 GI:9929282
KEYWORDS      60S ribosomal protein L26; atf1; isp4; sexual differentiation;
SOURCE      fission yeast.
ORGANISM      Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomycetes.
REFERENCE      1 (bases 1 to 14147)
AUTHORS      Wood,V., Rajandream,M.A., Barrell,B.G., Saunders,D. and Harris,D.
TITLE      Direct Submission
JOURNAL      Submitted (24-AUG-1999) European Schizosaccharomyces genome
sequencing project, Sanger Centre, The Wellcome Trust Genome
Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk
COMMENT      Notes:
Details of yeast sequencing at the Sanger Centre are available on
```

FEATURES

SOURCE

the World Wide Web.
(URL: http://www.sanger.ac.uk/Projects/S_pombe/)
during 1995 to 1996 about 66% of *S. pombe* chromosome 1 was
sequenced by the Sanger Centre. The sequencing of the *S. pombe*
genome is now being continued with funding from the European
Commission. Fourteen European sequencing laboratories, including
the Sanger Centre, are participating in the project.
Protein coding regions (CDS) have been predicted with the help of
computer analysis using the GeneFinder program in Pombase (an ACEDB
database) with additional predictions for the branch-acceptor sites
supplied by the program Sp3splice. CAUTION: It is possible that for
any individual CDS we may have underestimated or overestimated the
number of introns/exons or we may not have chosen the correct
splice donor/acceptor sites.
CDS are numbered using the following system eg SPBC25H2.01c. SP (*S.*
pombe), B (chromosome 2), c25H2 (cosmid name), .01 (first CDS), c
(complementary strand).
The more significant matches with motifs in the PROSITE database
are also included but some of these may be fortuitous.
The length in codons is given for each CDS.
IMPORTANT: This sequence MAY NOT be the entire insert of the
sequenced clone. It may be shorter because we only sequence
overlapping sections once, or longer, because we arrange for a
small overlap between neighbouring submissions.
Cosmid c29B5 is overlapped at the 3' end by cosmid c27, EMBL entry
SPBC27, accession number AL353866.
Location/Qualifiers

1..14147

/organism="Schizosaccharomyces pombe"

/strain="972h"

/db_xref="taxon:4896"

/chromosome="II"

/clone="cosmid c29B5"

/map="TIL"

1..101

/note="nominal overlap with SPBC83 *S. pombe* chromosome 2"

224..1924

/gene="atf1"

/note="atf1"

224..1924

/gene="atf1"

/note="SPBC29B5.01, len:567"

/label="atf1"

/codon_start=1

/product="transcription factor atf1"

/protein_id="CAC0510.1"

/db_xref="GI:995813"

/translation="MSPSPVNTSREPAVVAVNSGNATASSTOVPENNOSDSFAPSN
NSOQNOOSSTIAFWGAGSVANNPNADSGVTPFVGSILKLEYENPFPFHSFSTAS
VGQNPFLNRNPSLSNIPSGVPPAFATLLPVSSTIASPILSGARGIASPLGYPAMS
AFTRGTMHNPISAIDATLRPDYLNPSDAASAARSSGTGTPGVNEFRSLRPT
GAGPAPSPGTAHLGFHFDSDQFPDQYRTPRGRKPVVNGDSDFEGANAIV
GICLLSOVPODOOKLQOPISENDOASTANMLKQTOOTPDPSIRPFTONTNQ
AVGTGNPQASRTQOQPMYFMGSOQFNGMPSYGVIVNPADPSLTLKQTFDSGQNAE
NGSTINLQKTSNDMPNPTANSMPTVLENGTGYSTVSOEPPSANNOSPTSSINCKASE
SANTSTSGSSRRNSKNETDEEKRKFLERNRQAIAKQORRKNWLSNIOAKVEYEG
NENBILSAOVSALEELIVSLKTLIAHKDCPVAKNSAAVATVYISGDLAKXINLIG

1658..1825

/gene="atf1"

/note="Match to PF00170 bZIP, bZIP transcription factor

Score 48.62"

complement(2997..5354)

/gene="isp4"

/note="SPBC29B5.02c"

complement(2997..5354)

/gene="isp4"

/note="SPBC29B5.02c, len:786"

/codon_start=1

/label="isp4"

/product="sexual differentiation process protein isp4"

/protein_id="CAC0511.1"

/db_xref="GI:995814"

misc_feature

gene

CDS

1	misc_feature	6417..6705	/note="low complexity gene free region"
2	misc_feature	8379..8586	/note="region of unusual composition"
3	misc_feature	complement(110803..11183)	/note="region of unusual composition"
4	gene	/gene="rpl26"	
5	CDS	/note="SPBC2985.03c"	
6		/gene="rpl26"	
7		/note="SPBC2985.03c, len:127"	
8		/codon_start=1	
9		/label=rpl26	
10		/product="60s ribosomal protein 126"	
11		/protein_id="CAC05512.1"	
12		/db_xref="GI:9935815	
13		/translation="MKFSRDVTSRRKORAKHFGAPSSVRRVLMSAPLSKELREOYKI RSLPRRDDQITVIRGNSNGKREKITSYVRKKFLLIERVTRERKANGASAPVGDASK VYIKRLDKRKLIIYRKGGYK"	
14	misc_feature	complement(110866..11039)	
15		/gene="rpl26"	
16		/note="Match to PF00467 Ribosomal_L24, KOW motif Score 83.61"	
17	gene	complement(11868..13685)	
18	CDS	/gene="SPBC2985.04c"	
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21		/note="SPBC2985.04c, len:606"	
22		/codon_start=1	
23		/product="hypothetical protein similar to yeast YNL094W"	
24		/protein_id="CAC05513.1"	
25		/db_xref="GI:9935816"	
26		/translation="MFRSGRLPFGSESEPTINDLNSITTYPOCFISTGKGESEPKH ISVHGVAVVENPDNLNGLGRKDRMLNLRRYVGLPGRSKETGTPYRKKDEMNIOYV VDTRAOILNVNVRKQNDPDLSTSKRENDPPLSHRTPPDLOGNYYNVPBLSASR SWOYSGYIGSGFRKRLMTPSVNSQYISTGLACEEYFEERSLASLQRLKDFVLVYK IYADKNFEQKVAEEFNWATNVEGYFLIDIEVIPPYTKNKFVEAVLLOSTSEEDVYI KAYNSEVPLDRNGISLISDIDIVKNTRIEGRPKRGFTLLAPLNTQITIEGSDMF RYMNLNATVAFVNSPWOMLPTLSKFTNDNMPYISSIYLRHNGVLOINIEPAAR KRSLTLAISRLGDKIVLIGDNGEODLOIYAMACCFERRIIGTIRDMSPFCVL KQSTTKNSLPEVVOYMPKPAFTSPDPIKFTFTTTLKDVNDQESGSEYQLEKEDPYPL TFILHRTYTRIEVEDAKNTRKRPVOYVERHASKLENNHVLCDYCKHKCSNMEQDF VQAKRAGVILPHLPYIWMNGEPEPISFTDLKLSAFAS"	
27	misc_feature	13995..14147	
28		/note="nominal overlap with SPBC27 S. pombe chromosome 2"	
29	BASE COUNT	4573 a 2724 c 2550 g 4300 t	
30	ORIGIN		
31	Query Match	28.9%; Score 117.8; DB 8; Length 14147;	
32	Best Local Similarity	61.0%; Pred. No. 6.2e-21;	
33	Matches 191; Conservative	0; Mismatches 122; Indels 0; Gaps 0;	
34	96 atgaagattccaaagtgtatcgtctcgtcagaagaagcagagagaacatacttccaa 155		
35	11183 ATGAAGTCTCCAGGAGATCTACTAGCTCTGTCGCAAGCAGGAAGGCTCACTTGGC 11124		
36	156 gacacatcttcgttcagcgaataactatcagtggtgcacaccttgcacaaagaaactcgtacg 215		

QY	216	aaatacagcttcgtccttaccattcgcgaagaagacgaagatcatagttcgcga	275
Db	11063	CAATACAAAGATCGCTTCTCTTCACAGTGTGCTGATMGACCAAAATACATCGTATCCGTGTGT	11004
QY	276	gcttcaagggttagaagaagaagttaccacgctgtttatcgaagaataatccgatcat	335
Db	11003	TCCAACCAAGGTCGGGAAGCAAGATCATCCCTCCGCTACCGGTAACAGATTCCTCTCTCT	10944
QY	336	atcgaagagatgtaccagagaagaagaacgaatgtgaatgactgactcgtgtggaatacatca	395
Db	10943	ATTGAGCGGTGTACCCCGCAGAGAGCCGCAACGATGCTGCTGACCCGCTGGATTCAGACGC	10884
QY	396	tctaatgttgtta 408	
Db	10883	TCTAAGGTGTGCA 10871	
RESULT	7		
AC091511			
LOCUS	AC091511	97911 bp DNA	INV 09-JUN-2001
DEFINITION	Leishmania major chromosome 35 clone P860 strain Friedlin, complete sequence.		
ACCESSION	AC091511		
VERSION	AC091511.2	GI:14333935	
KEYWORDS	HTG.		
SOURCE	Leishmania major.		
ORGANISM	Leishmania major		
REFERENCE	1 (bases 1 to 97911)		
AUTHORS	Myler, P.J., Sisk, E., Cawthra, J., Nelson, S., Vogt, C., Robertson, L., McConagh, P., Ivens, A., Nguyen, D., Munden, H., Stuart, K., Mack, U., Marty, A., and Seyler, A.		
TITLE	Direct Submission		
JOURNAL	Submitted (27-APR-2001) Seattle Biomedical Research Institution, 4 Nickerson Street, Seattle, WA 98109-1651, USA		
REFERENCE	2 (bases 1 to 97911)		
AUTHORS	Myler, P.J., Sisk, E., Cawthra, J., Nelson, S., Vogt, C., Robertson, L., McConagh, P., Ivens, A., Nguyen, D., Munden, H., Stuart, K., Mack, U., Marty, A., and Seyler, A.		
TITLE	Direct Submission		
JOURNAL	Submitted (09-JUN-2001) Seattle Biomedical Research Institution, 4 Nickerson Street, Seattle, WA 98109-1651, USA		
COMMENT	On Jun 9, 2001 this sequence version replaced gi:13811913.		
FEATURES			
Source	Location/Qualifiers		
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	/organism="Leishmania major"		
	/strain="Friedlin"		
	/db_xref="taxon:5664"		
	/chromosome="35"		
	/clone="P860"		
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ORIGIN			
Query Match	27.0%: Score 110.2; DB 3; Length 97911;		
Best Local Similarity	61.8%: Pred. No. 5.1e-19;		
Matches 175; Conservative 0; Mismatches 108; Indels 0; Gaps 0;			
QY	123	lctagaagaacagagaaacatcatcttcaagacacatcttcgttaccgaatactc 182	
Db	66203	TCCCGCCGCAAGGCGCCGCGTGTGACGATTCAGGCGCCGAGCCATMGTCGCCGTGTCTC 66262	
QY	183	atgagtgcacctgtgtcgaagaactagatcagaatacagcgtgtctttaccatt 242	
Db	66263	ATTGACGCCCGCTCTCCAAAGACTGTGGCGCCCAAGTACAACGTGCGCATCCCGTG 66322	
QY	243	cgaagaagaacgaagatcatcatagtttcgcgagccttcaagggttagaagaagaatt 302	
Db	66323	CGCAAGGACGACGAGGTGATGTGTAAGCGGCGACCTTTCAAGGCGCGTGAAGGAAAGTG 66382	

QY 303 acaacggttcatcgaagaataatcgcatacatcagagaaatgacacgaagaaaagcg 362
Db 66383 ACGGCGTGTACCGCCCTCAAGTGGGTGATCTCCTATCATGATGAAGGGAACCCGAGAAAGCG 66442

QY 363 atatgaatgaactgaactctgfgaataatcaatcaatattg 405
Db 66443 AAGCGCTCCACCGGCGCGTGGCATCCATCCCTCCAACTCG 66485

RESULT	8			
CNS061DT				
LOCUS	CNS061DT	979 bp	DNA	SFS
DEFINITION	T7 end of clone AS0A019006 of library AS0A from strain CLIB 533 of <i>Saccharomyces bayanus</i> , sequence tagged site.			

VERSION	AL400167.1	GI:12155716
---------	------------	-------------

ORGANISM *Saccharomyces bayanus*

REFERENCE 1 (bases 1 to 979)

TITLE Genomic Exploration of the Hemiascomycetous Yeasts: 5.

PUBMED 11152880

Saurin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,

yeast species for molecular evolution studies(1)
 PMID: 1441407 (1) 3-13 (2000)

REFERENCE 3 (bases 1 to 979)

JOURNAL

COMMENT This STS is part of a random genomic sequencing program of thirteen yeast species: *Saccharomyces bayanus* var. *lvarum*, *Saccharomyces*

Saccharomyces kluyveri, *Kluyveromyces thermotolerans*, *Kluyveromyces fragilis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia pastoris*.

Candida tropicalis and *Yarrowia lipolytica*. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See

the other extremity of this insert.

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/organism="Saccharomyces bayanus"  
/strain="OTB 533"
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/db_xref="taxon:4931"  
/catalase="AC027018.06"
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    <530 >887

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RPL26B ; 60S large subunit ribosomal protein]

ORIGIN

Query Match	26.9%;	Score 109.8;	DB 11;	Length 979;
Best Local Similarity	60.0%;	Pred. No. 1.1e-18;		
Matches 183; Conservative	0;	Mismatches 122;	Indels 0;	Gaps 0.

104 ttccaaagtctgtatcgtctgctltagaagaagcagaggaaagcatacttcaagcacattc 163
|| || || || || || || || || || || || || || || || || || || || || ||
518 atttttaattacacgccttccttccttcacagaaagggccagaaaagggctcatttcagcgcccattc 577

164 ttcgtacgacgaattactcatgtgcaacctgtccaaggaaactacgtaagaaatcacg zc

224 ctttcttttaccntattcgaagaaagaaacgaagataatcataqttcgcagaaqcttcca 283

638 TATCAAGGCTTGGCAATCAGAAGAGAAGATGAAGTCTTGGTTGTTCGTCGTCCTCCAGAA 09

608 CCGCAGAGAGCTAAGATTCTTCTGTTTACAGATTGAAGTTTCTGTTCAAGTTGACCA 757

344 agtgcacagagaaagcgaatgtgaatcgactgtcaccctgtggaalacacaccacccaaagc

101 +++++ 108

b 818 TGT TA 822

RESULT 9
Y0733088

DEFINITION Sequence 409 from Patent WO01025550.
SEQUENCE AY073298

KEYWORDS . *Candida albicans*

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.

AUTHORS
Contreras, R. H., de Backer, M. D., Luyten, W. H., Malcolm, I. R.,
Nalissen, B. J. and Beekmans, R. J.

JOURNAL Patent: WO 0102550-A 409 11-JAN-2001
JANSSEN PHARMACEUTICA N.V. (BE)

```

source
1. .1348
/organism="Candida albicans"

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ORIGIN	BASE COUNT	512 a	194 c	196 g	440 l
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Matches	183;	conservative	0;	mismatches	122;	inserts	0;	delets	0
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976 TTATATAGAGCTTCTTCATCTCGTTCCTAAAGCTAGAAAGCTTATTTCACTGCTTCATC 10

164 tctgtacgacgaatacctaagtgcaaccatgccaaaggaaacacgg

224 ctttccttcttaccctattcgaagaaqaqaataatcatatgcttcgcgcgaqctttcaa 28

1096 TGTCAATCTTGGCCAATTAGACAAATGATGAAGTTTATGTTGTTAGAGGTTCTATTTAA 11

1156 ACCCTCTCAACGTAAGTTAATCTGTTTATAGATTGAAATTTCCTATTCAGTTCATTA 12

1156 AGGTTCTGAAGCTAAGTTAATCTGTTATAGATTGAATTGCTATTCAGTTGATAA 12

Oy	344 agtaccacgagaaaaagggaatgatctactcgtgggaatacatccatcaatcgt	403
Db	1216 ATTACAAAAAGAAAATCAATGTGCTTCTGTCCAAACAACATTCCATCAAAGT	1275
Oy	404 tttta 408	
Db	1276 TGTCA 1280	

RESULT	10
LOCUS	CNS01B90
DEFINITION	CNS01B90 480 bp mRNA
ACCESSION	AL113932
VERSION	AL113932.1 GI:5828551
KEYWORDS	CDNA library; nitrogen deprivation.
SOURCE	Botryoclinia fuckelliana.
ORGANISM	Botryoclinia fuckelliana
	PLN 02-SEP-1999
	T4 cDNA library under conditions of

REFERENCE AUTHORS TITLE JOURNAL	REFERENCE AUTHORS TITLE JOURNAL
(bases 1 to 480) Bition, F., Lewis, C., Fortini, D., Pradier, J.M. and Brygoo, Y. Direct Submission Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr, 78026 Versailles, France	(bases 1 to 480) Genoscope. Direct Submission Submitted (01-SEP-1999) Genoscope - Centre National de Séquençage

COMMENT The cDNA library to be analyzed within the framework of this project was created using a *Botrytis cinerea* strain which was grown under conditions of nitrogen deprivation, which is the normal situation for *B. cinerea* during its development on its host plant. The library was produced in an oriented direction, in the pSII vector.

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FEATURES
source      Location/Qualifiers
            1..480
            /organism="Botryotinia fuckeliana"
            /strain="74"
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            /note="Genoscope sequence ID : W24A1117"
BASE COUNT      132 a      128 c      116 g      104 t

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Query Match	26.1%;	Score 106.6;	DB 8;	Length 480;
Best Local Similarity	60.6%;	Pred. No. 8.1e-18;		
Matches 175; Conservative	0;	Mismatches 114;	Indels 0;	Gaps 0;

QY	120	tcgtctagaagaagaacgagaaagaactattcttcaagaccactctctctgaagcgaata	179
QY	121		
QY	122		
QY	123		
QY	124		
QY	125		
QY	126		
QY	127		
QY	128		
QY	129		
QY	130		
QY	131		
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QY	228		
QY	229		
QY	230		
QY	231		
QY	232		
QY	233		
QY	234		
QY	235		

RESULT	11
CNS01CFH	
Locus	
DEFINITION	CNS01CFH 506 bp mRNA PIN 02-SEP-1998
Accession	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation.
	nt1462

ACCESSION	AL115461
VERSION	AL115461.1
KEYWORDS	cdna library; nitrogen deprivation.
SOURCE	<i>Botryotinia fuckeliana</i> .
ORGANISM	<i>Botryotinia fuckeliana</i>

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 506)
Bittou, P., Lewis, C., Fortini, D., Pradier, J.M. and Brygoo, Y.
Direct Submission
Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr
76026 Versailles, France
2 (bases 1 to 506)
Genoscope.
Direct Submission
Submitted (01-SEP-1999) Genoscope - Centre National de Séquences

COMMENT The cDNA library to be analyzed within the framework of this project was created using a *Bolytis cinerea* strain which was grown under conditions of nitrogen deprivation, which is the normal situation for *B. cinerea* during its development on its host plant. The library was produced in an oriented direction, in the pBSII vector.

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FEATURES
source
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    1. 506
        /organism="Botryotinia fuckeliana"
        /strain="T4"
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        /note="Genoscope sequence ID : W54A061"
BASE COUNT
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Query Match	26.1%;	Score 106.6;	DB 8;	Length 506;
Best Local Similarity	60.6%;	Pred. No. 8e-18;		
Matches 175; Conservative	0;	Mismatches 114;	Indels 0;	Gaps 0

QY		120	tgtctagaagaaagcagnagaagaacataacttccaagcaaccattcttgtaacgaata	179
Dd		61	TCTTCAGAGAAGTCCCGCAGGCTCATTTTGATGCCCAATCAGGTGCAGACGTACC	120

QY 180 ctcattgagtcacccctgtctcaagaaactacgtacgaataacagctgttcttacct 239
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 Db 121 ATCATGAGCGCTCCTTTTGAGCAAGGAACCTCGTGAGAGTACAACTCCGCTCCATCCCA 180

DQ 240 attcgaaagaagacgaagcaatcatcagtctgcgagcttcctaagtgtagaagaaaa 299
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 ATCGAAAGGATGATGAGGTACCACTCGTTCGTGGTTCCAAACAAGGGCTCCAGGGAAG 240

DY 300 gttacaacgltgtatcgaagaatactcgatatactgaagagtgcaccagaaaaa 359
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Db 241 ATCACCTCCGTTACCGGTTCACAANAAGTGCATCAGCGAGCGTGCTCAAGAGAAG 300

QY 360 gcgatggaatgactgttacctgtggatatacatccatctaattgttca 408
 1 1111 1 1111 1 1111 1 1111 1 1111 1 1111 1 1111
 Db 301 TCCTCTGGACATCCGTTCCCTCGGTATCCACCACCATCCAAGTCA 349

RESULT	12			
LOCUS	CNS01972			
DEFINITION	CNS01972	540 bp	mRNA	PLN
ACCESSION	BT0175	cimerea strain	74	CNMA library under conditions of
VERSION	AL111303	nitrogen	deprivation.	
KEYWORDS	AL111303.1	GI:5825922		
	CNMA library; nitrogen	deprivation.		

[illegible]

REFERENCE	TITLE	AUTHORS	COMMENT
2	(bases 1 to 540)	Genoscope.	
1	Direct Submission		
Submitted (01-SEP-1999)	Genoscope - Centre National de Sequencage :		
CP 5706 91057 EVRY cedex - FRANCE	(E-mail : sequef@genoscope.cns.fr		
- Web : www.genoscope.cns.fr)			
The cDNA library to be analyzed within the framework of this			
project was created using a Botrytis cinerea strain which was grown			
under conditions of nitrogen deprivation, which is the normal			
situation for B. cinerea during its development on its host plant.			
The library was produced in an oriented direction, in the pBSII			
vector.			
location/Qualifiers			
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/organism="Botryotinia fuckeliana"			
/strain="r4"			
/db_xref="taxon:40559"			
/note="Genoscope sequence ID : W34H091"			
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ORIGIN			
Query Match	26.1%	Score 106.6;	DB 8; Length 540;
Best Local Similarity	60.6%	Pred. No. 8e-18;	
Matches	175;	Conservative	0; Mismatches 114; Indels 0; Gaps 0;
QY	120	tcgtatagaagaagacagagaaagacatacttcaagcacatcttctgtacagcagata	179
Db	64	ttcttcacagagaaatcccccagacgctatttcgattgcccccattccagcagcgtacc	123
QY	180	ccctagatgcaccccttgcacaagaatactagcagaaacacagcgttcgtcttacct	239
Db	124	atcattagcggcctctttgacagagaaatcccttgagaaagttacacagctccgtccatcca	183
QY	240	attcgaagaagaagaagaaatcatcatagtcgcgagcgttcaagagtgatagaagaata	299
Db	184	atcagaaagatgatagagaggtcacactcgttcgtggtttccaaagggcctccgaggaag	243
QY	300	gttcaacagctgttatcgaagaataatcgcgatactcagagagagtgaccagagaataa	359
Db	244	atccactccgcttaccgcttcataatnactgcgtccacgtcagcgcgtctcgaagagag	303
QY	360	ggcaatgcagatgacttacctgtggygaatacatcatcatatgttgtta	408
Db	304	ttccttgagacattccgttccctcgatnccaccatccaaaggtcatca	352
RESULT 14			
CNS01A0A	540 bp	mRNA	PLN 02-SEP-1999
LOCUS	Botrytis cinerea strain T4 cDNA library under conditions of		
DEFINITION	nitrogen deprivation.		
ACCESSION	AL113186		
VERSION	AL113186.1 GI:5827805		
KEYWORDS	CDNA library; nitrogen deprivation.		
SOURCE	Botryotinia fuckeliana.		
ORGANISM	Botryotinia fuckeliana		
REFERENCE	1 (bases 1 to 540)		
AUTHORS	Bilton,F., Levis,C., Fortini,D., Pradier,J.M. and Brygoo,Y.		
TITLE	Direct Submission		
JOURNAL	Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr,		
REFERENCE	78026 Versailles, France		
AUTHORS	2 (bases 1 to 540)		
TITLE	Genoscope.		
JOURNAL	Direct Submission		
COMMENT	Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage :		
	CP 5706 91057 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr		
	- Web : www.genoscope.cns.fr)		
	The cDNA library to be analyzed within the framework of this		
	project was created using a Botrytis cinerea strain which was grown		
	under conditions of nitrogen deprivation, which is the normal		

FEATURES

BASE COUNT	147	a	146	c	128	g	119	t
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Dh 56 TCCTCCAGGAAATCCCCCAGGCATTTCGTGGATGCCCATCCAGCGTACAGACTACC 115
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QY 180 ctcataagatgcaccctgtctccaaggaactacgtaagaataacaggttcgtttcttaacct 2339
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 Db 116 ATCATGACCGCTCTTTGAGCAAGGACTCCCGTGAGGAAGTACAACGTCCTCCATCCCA 175

QY 240 attcgaaaaagaagacgaagtcaatcatagttcgcgagcttcaaggtagagaagaaaa 299
|| |||| | | | | | | | | | | | |
db 176 ATCAGAAAGGATGATGAGGTCCACCACTGTCCTCGGCTTCCACCAACCCTGGCCGCCCTA 225

QY		gtttacaacgltcgcgaagaatalcgatcatatcagagagagtagaccagagaanaa	350
Db	236	attcacctccgcttaccgcttcataatcctgcgtacagtgtaacgctgctgtaagaagaag	295

Qy 360 gcgatgggaatgactgtacctgtgaggaaatacatcctaattgttga 408
 | ||||| ||||| ||||| ||||| ||||| |||||
Db 296 TCCTGTGACAAATCCGTTCCCGTCGGATGCCACCATTCAAGTATATA 344

RESULT	15
CNS01BT1	
LOCUS	
CNS01BT1	540 bp mRNA PLN 02-SEP-1999
DEFINITION	Botrytis cinerea strain T4 cDNA library under conditions of

accession nitrogen deprivation.
 AL114653
 version AL114653.1 GI:5829272
 keywords CDNA library; nitrogen deprivation.
 database GenBank

ORGANISM	REFERENCE
<i>Botryotinia fuckelliana</i>	1 (bases 1 to 540)
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Helotiales; Sclerotiniaceae; Botryotinia.	

AUTHORS Bilton, F., Lewis, C., Fortini, D., Pradier, J.M. and Brygoo, Y.
TITLE Direct Submission
JOURNAL Submitted (01-SEP-1999) Phyltopathologie, INRA, route de St Cyr
76026 Versailles, France

RECEIVED
AUTHORS
TITLE
JOURNAL
Direct Submission
Submitted (01-SEP-1999) Genoscope - Centre National de Sequençage
CP 5706 91057 Evry Evry - FRANCE
CP 5706 91057 Evry Evry - FRANCE

The cdna library to be analyzed within the framework of this project was created using a *Botrytis cinerea* strain which was grown under conditions of nitrogen deprivation, which is the normal situation for *B. cinerea* during its development on its host plant. The library was produced in an oriented direction, in the pBSII vector.

FEATURES
SOURCE

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Location/Qualifiers
1..540
/organism="Botryotinia fuckeliana"
/strain="T4"
/db_xref="taxon:40559"
/note="Genoscope sequence ID : W62D1111"
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Query Match	26.1%;	Score 106.6;	DB 8;	Length 540;
Best Local Similarity	60.6%;	Pred. No. 8e-18;		
Matches 175; Conservative	0;	Mismatches 114;	Indels 0;	Gaps 0;

Oy 120 tgcgtcagagaagaacgaggaagaacatacttccaaacacatcttcgtcaagaata 179
| | | | | | | | | | | | | | | | | |
Db 53 TCCCTCAGGAGAAGTCCCCGACGGTCATTTTGGATGCCCAATCCAGGTGACAGGTACC 112

Dy 180 cttatagatgtcaccccttccaagaactacgtacgaataaacgcttcgtcctaact 239
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 113 atcatagaggctcttttgacgaagaaactccgtgaagaactacaagctcgctccattcca 172

0y 240 attcgaagaagaaagaaatatactagttccgsgagcgttcaagggtatagaagaagaaa 299
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Db 173 ATCCAAAAGATGAAGAAGTACCATTGTTCTGTTCACAAACAAGGGCTCCGAGGGAAG 232

Oy	360	gcgaatggaatacttaccctgttggaatacattccatctaattatttta	408
Dd	233	ATCACCCTCGGTACCGTCGTAATTAGTGGTGCCACTGTGACCGTGTGTTAAAGCAAG	292

Db 293 TCCTTGACAAATCCGTTCCCGTGATCCACCAATCCAGAGTCATCA 341

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